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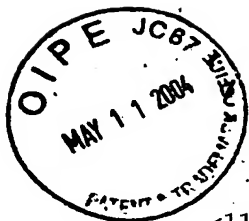
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279152RX
SEQUENCE LISTING

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<141> 2001-04-05

<150> 60/195,532

<151> 2000-04-07

<150> 60/247,014

<151> 2000-11-13

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<170> PatentIn Ver. 2.1

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Ala Leu Ser Asn Ser Asp Cys Val Leu Leu Cys Leu Ser Ile Ser Arg
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 65 70 75 80
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 100 105 110
 Trp Leu Ser Phe Phe Tyr Phe Val Lys Ile Ala Asn Phe Ser Tyr Pro
 115 120 125
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 145 150 155 160
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 165 170 175
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 180 185 190
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 Leu Thr Ala Thr Leu Leu Ile Leu Ser Leu Lys Arg His Thr Leu His
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Met Gly Ala Ile Lys Ala Ile Ser Tyr Phe Leu Ile Leu Tyr Ile Phe
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Asn Ala Val Ala Leu Phe Ile Tyr Leu Ser Asn Met Phe Asp Ile Asn
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Arg Gly Lys Thr Leu Pro Thr Gly Asp Arg Ile Met Leu Met Leu Ser

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 Phe Lys Val Ile Thr Val Phe Leu Asn His Ser Asn Leu Trp Phe Ala
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 Ala Trp Leu Lys Val Phe Tyr Cys Leu Arg Ile Ala Asn Phe Asn His
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 Pro Leu Phe Phe Leu Met Lys Arg Lys Ile Ile Val Leu Met Pro Trp
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 165 170 175
 Ser Ser Asn Ser Thr Glu Lys Lys Tyr Phe Ser Glu Thr Asn Met Val
 180 185 190
 Asn Leu Val Phe Phe Tyr Asn Met Gly Ile Phe Val Pro Leu Ile Met
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 Phe Ile Leu Ala Ala Thr Leu Leu Ile Leu Ser Leu Lys Arg His Thr
 210 215 220
 Leu His Met Gly Ser Asn Ala Thr Gly Ser Arg Asp Pro Ser Met Lys
 225 230 235 240
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 245 250 255
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 260 265 270
 Thr Tyr Ser Ser Trp Asn Ile Leu Cys Lys Ile Ile Met Ala Ala Tyr
 275 280 285
 Pro Ala Gly His Ser Val Gln Leu Ile Leu Gly Asn Pro Gly Leu Arg
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 Arg Thr Thr Ala Tyr Asn Ile Trp Ala Val Ile Asn His Phe Ser Asn
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 Trp Leu Ala Thr Thr Leu Ser Ile Phe Tyr Leu Leu Lys Ile Ala Asn
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 Phe Ser Asn Phe Ile Phe Leu His Leu Lys Arg Arg Val Lys Ser Val
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 Phe Val Ile Asn Met Asn Glu Ile Val Arg Thr Lys Glu Phe Glu Gly
 145 150 155 160
 Asn Met Thr Trp Lys Ile Lys Leu Lys Ser Ala Met Tyr Phe Ser Asn
 165 170 175
 Met Thr Val Thr Met Val Ala Asn Leu Val Pro Phe Thr Leu Thr Leu
 180 185 190
 Leu Ser Phe Met Leu Leu Ile Cys Ser Leu Cys Lys His Leu Lys Lys
 195 200 205
 Met Gln Leu His Gly Lys Gly Ser Gln Asp Pro Ser Thr Lys Val His
 210 215 220

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Ile Lys Ala Leu Gln Thr Val Ile Ser Phe Leu Leu Leu Cys Ala Ile
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Tyr Phe Leu Ser Ile Met Ile Ser Val Trp Ser Phe Gly Ser Leu Glu
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Asn Lys Pro Val Phe Met Phe Cys Lys Ala Ile Arg Phe Ser Tyr Pro
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Ser Ile His Pro Phe Ile Leu Ile Trp Gly Asn Lys Lys Leu Lys Gln
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Ala Ala Leu Ala Val Ser Arg Val Gly Leu Leu Trp Val Ile Leu Leu
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His Trp Tyr Ser Thr Val Leu Asn Pro Thr Ser Ser Asn Leu Lys Val
 65 70 75 80

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Ile Ile Phe Ile Ser₈₅ Asn Ala Trp Ala Val₉₀ Thr Asn His Phe Ser₉₅ Ile
 Trp Leu Ala Thr₁₀₀ Ser Leu Ser Ile Phe Tyr Leu Leu Lys Ile₁₁₀ Val Asn
 Phe Ser Arg₁₁₅ Leu Ile Phe His₁₂₀ Leu Lys Arg Lys Ala₁₂₅ Lys Ser Val
 Val₁₃₀ Leu Val Ile Val Leu Gly₁₃₅ Ser Leu Phe Phe₁₄₀ Leu Val Cys His Leu
 Val₁₄₅ Met Lys His Thr₁₅₀ Tyr Ile Asn Val Trp Thr₁₅₅ Glu Glu Cys Glu Gly₁₆₀
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 Leu Thr Val₁₈₀ Ala Met Leu Ala Asn₁₈₅ Leu Ile Pro Phe Thr₁₉₀ Leu Thr Leu
 Ile Ser Phe₁₉₅ Leu Leu Leu Ile Tyr₂₀₀ Ser Leu Cys Lys His₂₀₅ Leu Lys Lys
 Met Gln₂₁₀ Leu His Gly Lys₂₁₅ Gly Ser Gln Asp Pro Ser₂₂₀ Thr Lys Ile His
 Ile₂₂₅ Lys Ala Leu Gln Thr₂₃₀ Val Thr Ser Phe₂₃₅ Leu Ile Leu Leu Ala Ile₂₄₀
 Tyr Phe Leu Cys₂₄₅ Leu Ile Ile Ser Phe₂₅₀ Trp Asn Phe Lys Met₂₅₅ Arg Pro
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 Ile Lys Ala Leu Gln Thr Val Thr Ser Phe Leu Met Leu Phe Ala Ile
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<210> 16
 <211> 299
 <212> PRT
 <213> Homo sapiens

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<400> 16

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 20 25 30
 Ile Asp Trp Val Lys Arg Lys Lys Ile Ser Ser Ala Asp Gln Ile Leu
 35 40 45
 Thr Ala Leu Ala Val Ser Arg Ile Gly Leu Leu Trp Ala Leu Leu Leu
 50 55 60
 Asn Trp Tyr Leu Thr Val Leu Asn Pro Ala Phe Tyr Ser Val Glu Leu
 65 70 75 80
 Arg Ile Thr Ser Tyr Asn Ala Trp Val Val Thr Asn His Phe Ser Met
 85 90 95
 Trp Leu Ala Ala Asn Leu Ser Ile Phe Tyr Leu Leu Lys Ile Ala Asn
 100 105 110
 Phe Ser Asn Leu Leu Phe Leu His Leu Lys Arg Arg Val Arg Ser Val
 115 120 125
 Ile Leu Val Ile Leu Leu Gly Thr Leu Ile Phe Leu Val Cys His Leu
 130 135 140
 Leu Val Ala Asn Met Asp Glu Ser Met Trp Ala Glu Glu Tyr Glu Gly
 145 150 155 160
 Asn Met Thr Gly Lys Met Lys Leu Arg Asn Thr Val His Leu Ser Tyr
 165 170 175
 Leu Thr Val Thr Thr Leu Trp Ser Phe Ile Pro Phe Thr Leu Ser Leu
 180 185 190
 Ile Ser Phe Leu Met Leu Ile Cys Ser Leu Cys Lys His Leu Lys Lys
 195 200 205
 Met Gln Leu His Gly Glu Gly Ser Gln Asp Leu Ser Thr Lys Val His
 210 215 220
 Ile Lys Ala Leu Gln Thr Leu Ile Ser Phe Leu Leu Leu Cys Ala Ile
 225 230 235 240
 Phe Phe Leu Phe Leu Ile Val Ser Val Trp Ser Pro Arg Arg Leu Arg
 245 250 255
 Asn Asp Pro Val Val Met Val Ser Lys Ala Val Gly Asn Ile Tyr Leu
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<210> 17

<211> 924

<212> DNA

<213> Homo sapiens

<400> 17

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<210> 18

<211> 307

<212> PRT

<213> Homo sapiens

<400> 18

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Ser Leu Leu Gly Ile Ala Ala Asn Gly Phe Ile Val Leu Val Leu Gly
          20           25           30
Arg Glu Trp Leu Arg Tyr Gly Arg Leu Leu Pro Leu Asp Met Ile Leu
          35           40           45
Ile Ser Leu Gly Ala Ser Arg Phe Cys Leu Gln Leu Val Gly Thr Val
          50           55           60
His Asn Phe Tyr Tyr Ser Ala Gln Lys Val Glu Tyr Ser Gly Gly Leu
          65           70           75           80
Gly Arg Gln Phe Phe His Leu His Trp His Phe Leu Asn Ser Ala Thr
          85           90           95
Phe Trp Phe Cys Ser Trp Leu Ser Val Leu Phe Cys Val Lys Ile Ala
          100          105          110
Asn Ile Thr His Ser Thr Phe Leu Trp Leu Lys Trp Arg Phe Pro Gly
          115          120          125
Trp Val Pro Trp Leu Leu Leu Gly Ser Val Leu Ile Ser Phe Ile Ile
          130          135          140
Thr Leu Leu Phe Phe Trp Val Asn Tyr Pro Val Tyr Gln Glu Phe Leu
          145          150          155          160
Ile Arg Lys Phe Ser Gly Asn Met Thr Tyr Lys Trp Asn Thr Arg Ile
          165          170          175
Glu Thr Tyr Tyr Phe Pro Ser Leu Lys Leu Val Ile Trp Ser Ile Pro
          180          185          190

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Phe Ser Val Phe Leu Val Ser Ile Met Leu Leu Ile Asn Ser Leu Arg
 195 200 205

Arg His Thr Gln Arg Met Gln His Asn Gly His Ser Leu Gln Asp Pro
 210 215 220

Ser Thr Gln Ala His Thr Arg Ala Leu Lys Ser Leu Ile Ser Phe Leu
 225 230 235 240

Ile Leu Tyr Ala Leu Ser Phe Leu Ser Leu Ile Ile Asp Ala Ala Lys
 245 250 255

Phe Ile Ser Met Gln Asn Asp Phe Tyr Trp Pro Trp Gln Ile Ala Val
 260 265 270

Tyr Leu Cys Ile Ser Val His Pro Phe Ile Leu Ile Phe Ser Asn Leu
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Lys Leu Arg Ser Val Phe Ser Gln Leu Leu Leu Leu Ala Arg Gly Phe
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Trp Val Ala
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<210> 19
 <211> 930
 <212> DNA
 <213> Homo sapiens

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<210> 20
 <211> 309
 <212> PRT
 <213> Homo sapiens

<400> 20

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Phe Val Ile Gly Asn Phe Ala Asn Gly Phe Ile Ala Leu Val Asn Ser
 20 25 30

Ile Glu Trp Phe Lys Arg Gln Lys Ile Ser Phe Ala Asp Gln Ile Leu
 35 40 45

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Thr Ala Leu Ala Val Ser Arg Val Gly Leu Leu Trp Val Leu Val Leu
 50 55 60
 Asn Trp Tyr Ala Thr Glu Leu Asn Pro Ala Phe Asn Ser Ile Glu Val
 65 70 75 80
 Arg Ile Thr Ala Tyr Asn Val Trp Ala Val Ile Asn His Phe Ser Asn
 85 90 95
 Trp Leu Ala Thr Ser Leu Ser Ile Phe Tyr Leu Leu Lys Ile Ala Asn
 100 105 110
 Phe Ser Asn Leu Ile Phe Leu His Leu Lys Arg Arg Val Lys Ser Val
 115 120 125
 Val Leu Val Ile Leu Leu Gly Pro Leu Leu Phe Leu Val Cys His Leu
 130 135 140
 Phe Val Ile Asn Met Asn Gln Ile Ile Trp Thr Lys Glu Tyr Glu Gly
 145 150 155 160
 Asn Met Thr Trp Lys Ile Lys Leu Arg Ser Ala Met Tyr Leu Ser Asn
 165 170 175
 Thr Thr Val Thr Ile Leu Ala Asn Leu Val Pro Phe Thr Leu Thr Leu
 180 185 190
 Ile Ser Phe Leu Leu Leu Ile Cys Ser Leu Cys Lys His Leu Lys Lys
 195 200 205
 Met Gln Leu His Gly Lys Gly Ser Gln Asp Pro Ser Met Lys Val His
 210 215 220
 Ile Lys Ala Leu Gln Thr Val Thr Ser Phe Leu Leu Leu Cys Ala Ile
 225 230 235 240
 Tyr Phe Leu Ser Ile Ile Met Ser Val Trp Ser Phe Glu Ser Leu Glu
 245 250 255
 Asn Lys Pro Val Phe Met Phe Cys Glu Ala Ile Ala Phe Ser Tyr Pro
 260 265 270
 Ser Thr His Pro Phe Ile Leu Ile Trp Gly Asn Lys Lys Leu Lys Gln
 275 280 285
 Thr Phe Leu Ser Val Leu Trp His Val Arg Tyr Trp Val Lys Gly Glu
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 Lys Pro Ser Ser Ser
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 <212> DNA
 <213> Homo sapiens

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 <212> DNA
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<210> 24
 <211> 303

279152RX

<212> PRT
<213> Mus sp.

<400> 24

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Cys Tyr Asp Leu Phe Lys Ser Arg Thr Phe Leu Ile Leu Gln Thr Leu
          35          40          45
Leu Met Cys Thr Gly Leu Ser Arg Leu Gly Leu Gln Ile Met Leu Met
          50          55          60
Thr Gln Ser Phe Phe Ser Val Phe Phe Pro Tyr Ser Tyr Glu Glu Asn
          65          70          75          80
Ile Tyr Ser Ser Asp Ile Met Phe Val Trp Met Phe Phe Ser Ser Ile
          85          90          95
Gly Leu Trp Phe Ala Thr Cys Leu Ser Val Phe Tyr Cys Leu Lys Ile
          100          105          110
Ser Gly Phe Thr Pro Pro Trp Phe Leu Trp Leu Lys Phe Arg Ile Ser
          115          120          125
Lys Leu Ile Phe Trp Leu Leu Leu Gly Ser Leu Leu Ala Ser Leu Gly
          130          135          140
Thr Ala Thr Val Cys Ile Glu Val Gly Phe Pro Leu Ile Glu Asp Gly
          145          150          155          160
Tyr Val Leu Arg Asn Ala Gly Leu Asn Asp Ser Asn Ala Lys Leu Val
          165          170          175
Arg Asn Asn Asp Leu Leu Leu Ile Asn Leu Ile Leu Leu Leu Pro Leu
          180          185          190
Ser Val Phe Val Met Cys Thr Ser Met Leu Phe Val Ser Leu Tyr Lys
          195          200          205
His Met His Trp Met Gln Ser Glu Ser His Lys Leu Ser Ser Ala Arg
          210          215          220
Thr Glu Ala His Ile Asn Ala Leu Lys Thr Val Thr Thr Phe Phe Cys
          225          230          235          240
Phe Phe Val Ser Tyr Phe Ala Ala Phe Met Ala Asn Met Thr Phe Arg
          245          250          255
Ile Pro Tyr Arg Ser His Gln Phe Phe Val Val Lys Glu Ile Met Ala
          260          265          270
Ala Tyr Pro Ala Gly His Ser Val Ile Ile Val Leu Ser Asn Ser Lys
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Phe Lys Asp Leu Phe Arg Arg Met Ile Cys Leu Gln Lys Glu Glu
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<210> 25

279152RX

<211> 20
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<220>
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<222> (3)
<223> Ile, Val or Leu

<220>
<221> MOD_RES
<222> (4)
<223> Val or Leu

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<222> (6)
<223> Ile or Val

<220>
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<222> (7)
<223> Leu or Val

<220>
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<220>
<221> MOD_RES
<222> (13)
<223> Val or Ala

<220>
<221> MOD_RES
<222> (18)
<223> Ile or Met

<220>
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Cys Xaa Asp Trp
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<210> 26
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<221> MOD_RES

279152RX

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<220>
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<223> Phe or Leu

<220>
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<223> Ile or Leu

<220>
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<222> (5)
<223> Thr or Ile

<220>
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<223> Gly, Ala or Ser

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<222> (13)
<223> Cys, Gly or Phe

<220>
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<210> 27
<211> 13
<212> PRT
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<220>
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<223> Ser, Thr or Asn

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<223> Leu, Ile or Val

<220>
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<223> Phe or Leu

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 <223> Ala or Thr

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<210> 28
 <211> 18
 <212> PRT
 <213> Artificial Sequence

<220>
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<220>
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 <223> Trp or Tyr

279152RX

<220>

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sequence

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Leu Lys

<210> 29

<211> 14

<212> PRT

<213> Artificial Sequence

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<221> MOD_RES

<222> (4)

<223> Ile, Phe or Val

<220>

<221> MOD_RES

<222> (8)

<223> Lys or Arg

<220>

<221> MOD_RES

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<223> Ser or Thr

<220>

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<223> Lys or Arg

<220>

<221> MOD_RES

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<223> Gln or Lys

<220>

<221> MOD_RES

<222> (13)

<223> Met or Ile

<220>

<221> MOD_RES

<222> (14)

<223> Gln or Lys

<220>

<223> Description of Artificial Sequence: Consensus
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<210> 30

<211> 14

279152RX

<212> PRT
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<223> Lys or Arg

<220>
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<222> (14)
<223> Gln or Arg

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<210> 31
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide translocation domain

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Thr Gly Val Val
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